

SPECIFICATION AMENDMENTS

Please replace the paragraph beginning at page 19, line 17, with the following rewritten paragraph:

The BLAST software suite, freely available sequence comparison algorithms (NCBI, Bethesda MD; <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>), includes various sequence analysis programs including "blastn" that is used to align nucleic acid molecules and BLAST 2 that is used for direct pairwise comparison of either nucleic or amino acid molecules. BLAST programs are commonly used with gap and other parameters set to default settings, e.g.: Matrix: BLOSUM62; Reward for match: 1; Penalty for mismatch: -2; Open Gap: 5 and Extension Gap: 2 penalties; Gap x drop-off: 50; Expect: 10; Word Size: 11; and Filter: on. Identity or similarity is measured over the entire length of a sequence or some smaller portion thereof. Brenner *et al.* (1998; Proc Natl Acad Sci 95:6073-6078, incorporated herein by reference) analyzed the BLAST for its ability to identify structural homologs by sequence identity and found 30% identity is a reliable threshold for sequence alignments of at least 150 residues and 40%, for alignments of at least 70 residues.

Please replace the paragraph beginning at page 20, line 23, with the following rewritten paragraph:

Following assembly, templates were subjected to BLAST, motif, and other functional analyses and categorized in protein hierarchies using methods described in USSN 08/812,290 and USSN 08/811,758, both filed March 6, 1997; in USSN 08/947,845, filed October 9, 1997; and in USSN 09/034,807, filed March 4, 1998. Then templates were analyzed by translating each template in all three forward reading frames and searching each translation against the PFAM database of hidden Markov model-based protein families and domains using the HMMER software package (Washington University School of Medicine, St. Louis MO; <http://pfam.wustl.edu/>).

Please amend the Table beginning at p. 22, line 13 as follows:

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 |
|--------------|----|----|----|---|----|---|----|---|---|----|----|----|----|----|----|----|----|----|----|----|
| 1 Lipase | | | | | | | | | | | | | | | | | | | | |
| 2 Colipase | 11 | | | | | | | | | | | | | | | | | | | |
| 3 Insulin | 11 | 17 | | | | | | | | | | | | | | | | | | |
| 4 Reg-1 beta | 5 | 5 | 5 | | | | | | | | | | | | | | | | | |
| 5 Reg-1 | 9 | 10 | 12 | 5 | | | | | | | | | | | | | | | | |
| 6 Reg- | 7 | 6 | 6 | 7 | 6 | | | | | | | | | | | | | | | |
| 7 Glucagon | 9 | 11 | 16 | 5 | 10 | 6 | | | | | | | | | | | | | | |
| 8 HiAPP | 5 | 4 | 4 | 7 | 4 | 6 | 4 | | | | | | | | | | | | | |
| 9 2091133 | 5 | 4 | 4 | 4 | 2 | 4 | 2 | 6 | | | | | | | | | | | | |
| 10 3836037 | 5 | 5 | 5 | 4 | 5 | 4 | 5 | 4 | 4 | | | | | | | | | | | |
| 11 3833667 | 5 | 5 | 5 | 4 | 5 | 4 | 5 | 4 | 4 | 7 | | | | | | | | | | |
| 12 3664676 | 3 | 5 | 5 | 0 | 5 | 0 | 5 | 0 | 0 | 2 | 2 | | | | | | | | | |
| 13 3835361 | 5 | 5 | 5 | 2 | 5 | 2 | 5 | 2 | 2 | 4 | 4 | 4 | | | | | | | | |
| 14 884692 | 3 | 5 | 5 | 2 | 5 | 2 | 5 | 2 | 2 | 2 | 2 | 4 | 4 | | | | | | | |
| 15 2383628 | 14 | 16 | 16 | 5 | 10 | 7 | 12 | 5 | 5 | 5 | 5 | 3 | 5 | 3 | | | | | | |
| 16 888246 | 7 | 6 | 6 | 4 | 4 | 4 | 4 | 4 | 6 | 7 | 7 | 2 | 4 | 2 | 7 | | | | | |
| 17 2774542 | 8 | 7 | 7 | 4 | 7 | 6 | 8 | 4 | 4 | 4 | 4 | 2 | 4 | 2 | 9 | 6 | | | | |
| 18 888309 | 5 | 5 | 5 | 4 | 5 | 4 | 5 | 4 | 4 | 7 | 7 | 2 | 4 | 2 | 5 | 7 | 4 | | | |
| 19 951335 | 12 | 11 | 11 | 5 | 10 | 7 | 8 | 4 | 4 | 5 | 5 | 3 | 5 | 3 | 13 | 7 | 8 | 5 | | |
| 20 2777115 | 11 | 10 | 10 | 3 | 7 | 3 | 7 | 3 | 5 | 6 | 6 | 3 | 6 | 3 | 12 | 8 | 7 | 6 | 10 | |
| 21 2075919 | 11 | 12 | 12 | 5 | 7 | 7 | 7 | 7 | 7 | 5 | 5 | 3 | 5 | 3 | 12 | 7 | 9 | 5 | 13 | 8 |